



PCT

## RAW SEQUENCE LISTING

DATE: 07/07/2004

PATENT APPLICATION: US/10/088,703A

TIME: 11:15:49

Input Set : A:\Sequence Listing for I0308.70002US00.txt

Output Set: N:\CRF4\07072004\J088703A.raw

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3 <110> APPLICANT: Isis Innovation Limited
4     Beth Israel Deaconess Medical Center, Inc.
5     Donnadieu, Emmanuel
6     Jouvin, Marie-Helene
7     Kinet, Jean-Pierre
8     Cookson, William
9     Moffatt, Miriam Fleur
11 <120> TITLE OF INVENTION: MODULATION OF IgE RECEPTOR CELL SURFACE EXPRESSION
13 <130> FILE REFERENCE: I00308/70002
15 <140> CURRENT APPLICATION NUMBER: US 10/088,703A
16 <141> CURRENT FILING DATE: 2002-03-21
18 <150> PRIOR APPLICATION NUMBER: PCT/US00/25877
19 <151> PRIOR FILING DATE: 2000-09-21
21 <150> PRIOR APPLICATION NUMBER: US 60/154,924
22 <151> PRIOR FILING DATE: 1999-09-21
24 <160> NUMBER OF SEQ ID NOS: 9
26 <170> SOFTWARE: PatentIn version 3.0
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29 <211> LENGTH: 3729
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
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42 agt aat agg aga gca aat ctt gct ctc cca cag gag cct tcc agt gtg      162
43 Ser Asn Arg Arg Ala Asn Leu Ala Leu Pro Gln Glu Pro Ser Ser Val
44 5                               10                               15                               20
45 cct gca ttt gaa gtc ttg gaa ata tct ccc cag gaa gta tct tca ggc      210
46 Pro Ala Phe Glu Val Leu Glu Ile Ser Pro Gln Glu Val Ser Ser Gly
47                               25                               30                               35
48 aga cta ttg aag tcg gcc tca tcc cca cca ctg cat aca tgg ctg aca      258
49 Arg Leu Leu Lys Ser Ala Ser Ser Pro Pro Leu His Thr Trp Leu Thr
50                               40                               45                               50
51 gtt ttg aaa aaa gag cag gag ttc ctg ggg gta aca caa att ctg act      306
52 Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr Gln Ile Leu Thr
53                               55                               60                               65
54 gct atg ata tgc ctt tgt ttt gga aca gtt gtc tgc tct gta ctt gat      354
55 Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys Ser Val Leu Asp

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57 att tca cac att gag gga gac att ttt tca tca ttt aaa gca ggt tat      402
58 Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe Lys Ala Gly Tyr
59 85      90      95      100
60 cca ttc tgg gga gcc ata ttt ttt tct att tct gga atg ttg tca att      450
61 Pro Phe Trp Gly Ala Ile Phe Phe Ser Ile Ser Gly Met Leu Ser Ile
62      105      110      115
63 ata tct gaa agg aga aat gca aca tat ctg gtg aga gga agc ctg gga      498
64 Ile Ser Glu Arg Arg Asn Ala Thr Tyr Leu Val Arg Gly Ser Leu Gly
65      120      125      130
66 gca aac act gcc agc agc ata gct ggg gga acg gga att acc atc ctg      546
67 Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly Ile Thr Ile Leu
68      135      140      145
69 atc atc aac ctg aag aag agc ttg gcc tat atc cac atc cac agt tgc      594
70 Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His Ile His Ser Cys
71      150      155      160
72 cag aaa ttt ttt gag acc aag tgc ttt atg gct tcc ttt tcc act gaa      642
73 Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser Phe Ser Thr Glu
74 165      170      175      180
75 att gta gtg atg atg ctg ttt ctc acc att ctg gga ctt ggt agt gct      690
76 Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly Leu Gly Ser Ala
77      185      190      195
78 gtg tca ctc aca atc tgt gga gct ggg gaa gaa ctc aaa gga aac aag      738
79 Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu Lys Gly Asn Lys
80      200      205      210
81 gtt cca gag gat cgt gtt tat gaa gaa tta aac ata tat tca gct act      786
82 Val Pro Glu Asp Arg Val Tyr Glu Glu Leu Asn Ile Tyr Ser Ala Thr
83      215      220      225
84 tac agt gag ttg gaa gac cca ggg gaa atg tct cct ccc att gat tta      834
85 Tyr Ser Glu Leu Glu Asp Pro Gly Glu Met Ser Pro Pro Ile Asp Leu
86      230      235      240
87 taa gaatcacgtg tccagaacac tctgattcac agccaaggat ccagaaggcc      887
88 aagggttttgt taaggggcta ctggaaaaat ttctattctc tccacagcct gctgggttta      947
89 cattagattt attcgctga taagaatatt ttgtttctgc tgcttctgtc caccttaata      1007
90 tgctccttct attttagat atgatagact cctatttttc ttgttttata ttatgaccac      1067
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96 gacatgaagt ttataaaga tctgtataat tgcctgaatc accagcacat tcatgacat      1427
97 gatattatatt gcagattgac aagtaggaag tgggggaactt ttattaagtt actcgttgtc      1487
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99 atgttttagtg aaacatttgt gaaaaaagaa gactaaatta agacctgagc tgaataaag      1607
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102 cgtttgagtc taagatgaaa ggagaacact ggttatgttg atagaatgat aaaaagggtc      1787
103 gggcgcgag gctcacgcct gtaatcccag ccctttggga ggccgaggtg ggcagatcac      1847
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107 cagtgcactc cagccttggg gacaatggga gactccatct caaaaaaaaaa aaaaaaaaaa 2087
108 aaaagataaa aagtcagaaa tctgaaaagt ggaggaagag tacaaataga cctaaattaa 2147
109 gtctcatttt ttggctttga ttttggggag acaaagggaa atgcagccat agagggcctg 2207
110 atgacatcca atacatgagt tctggtaaag ataaaatttg atacacgggt tgggtgtcatt 2267
111 ataagagaaa tcattattaa atgaagcaag ttaacactct aagagaatta ttttgagata 2327
112 gaagtgaagc taagctaaac ttcacatgcc tataattgga gggaaaaact aaggataaaa 2387
113 tctagcctag aagatacaat aattagtcac aaacatgcat tgtgaaactg tagagagcag 2447
114 gtagcccaaa atagagaaaag attagataaa gagaaaataa gtatccatca gagacagtat 2507
115 ctctaggctt gggcaagaga aaagtccaca gtgataagca actccaccta aggcataaat 2567
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133 ttgtgacctc cttatgtatt ctcaattacc tgtatttgtg caataaattg gaataatgta 3647
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137 &lt;210&gt; SEQ ID NO: 2

138 &lt;211&gt; LENGTH: 244

139 &lt;212&gt; TYPE: PRT

140 &lt;213&gt; ORGANISM: Homo sapiens

142 &lt;400&gt; SEQUENCE: 2

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149 Thr Trp Leu Thr Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr
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159 Gly Ser Leu Gly Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly
160          130          135          140
161 Ile Thr Ile Leu Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His
162 145          150          155          160
163 Ile His Ser Cys Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser
164          165          170          175
165 Phe Ser Thr Glu Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly
166          180          185          190
167 Leu Gly Ser Ala Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu
168          195          200          205
169 Lys Gly Asn Lys Val Pro Glu Asp Arg Val Tyr Glu Glu Leu Asn Ile
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187                               Met Asp Thr Glu
188                               1
189 agt aat agg aga gca aat ctt gct ctc cca cag gag cct tcc agt gtg      162
190 Ser Asn Arg Arg Ala Asn Leu Ala Leu Pro Gln Glu Pro Ser Ser Val
191 5          10          15          20
192 cct gca ttt gaa gtc ttg gaa ata tct ccc cag gaa gta tct tca ggc      210
193 Pro Ala Phe Glu Val Leu Glu Ile Ser Pro Gln Glu Val Ser Ser Gly
194          25          30          35
195 aga cta ttg aag tcg gcc tca tcc cca cca ctg cat aca tgg ctg aca      258
196 Arg Leu Leu Lys Ser Ala Ser Ser Pro Pro Leu His Thr Trp Leu Thr
197          40          45          50
198 gtt ttg aaa aaa gag cag gag ttc ctg ggg gta aca caa att ctg act      306
199 Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr Gln Ile Leu Thr
200          55          60          65
201 gct atg ata tgc ctt tgt ttt gga aca gtt gtc tgc tct gta ctt gat      354
202 Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys Ser Val Leu Asp
203          70          75          80
204 att tca cac att gag gga gac att ttt tca tca ttt aaa gca ggt tat      402
205 Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe Lys Ala Gly Tyr
206 85          90          95          100
207 cca ttc tgg gga gcc ata ttt ttt tct att tct gga atg ttg tca att      450

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211	Ile	Ser	Glu	Arg	Arg	Asn	Ala	Thr	Tyr	Leu	Val	Arg	Gly	Ser	Leu	Gly	
212					120					125					130		
213	gca	aac	act	gcc	agc	agc	ata	gct	ggg	gga	acg	gga	att	acc	atc	ctg	546
214	Ala	Asn	Thr	Ala	Ser	Ser	Ile	Ala	Gly	Gly	Thr	Gly	Ile	Thr	Ile	Leu	
215					135					140					145		
216	atc	atc	aac	ctg	aag	aag	agc	ttg	gcc	tat	atc	cac	atc	cac	agt	tgc	594
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218					150					155					160		
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220	Gln	Lys	Phe	Phe	Glu	Thr	Lys	Cys	Phe	Met	Ala	Ser	Phe	Ser	Thr	Val	
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229	ggactgggtca	gatggtaggg	agatgaaaac	aggagatgct	ataagaaaat	aaacttttgg											990
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